

Spacing Between Adjacent Peaks in the Raw Data  
(M13, T's T=6% 60C, Long Gel)

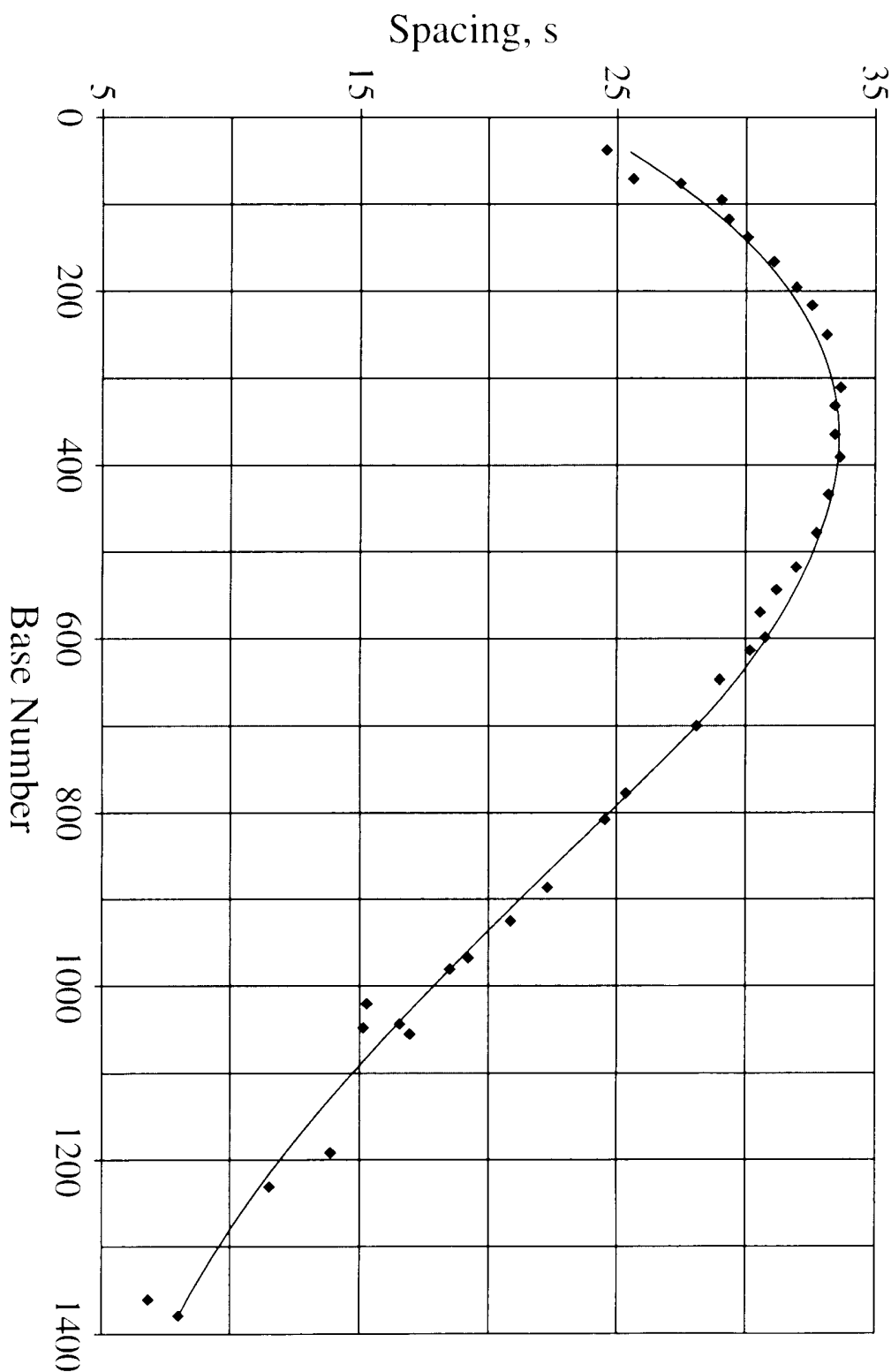
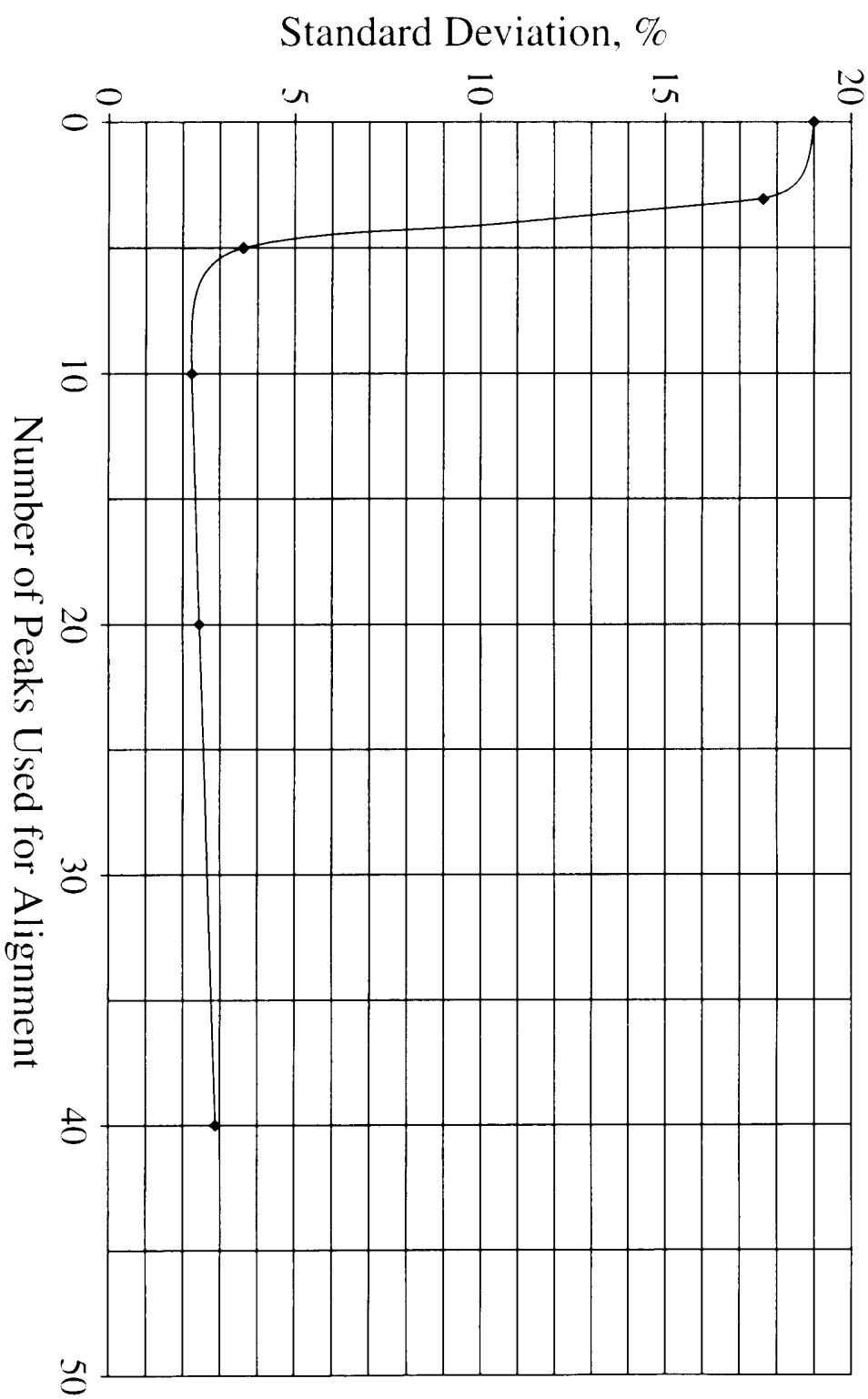


FIG. 1



Standard Deviation (%) of the Spacing Between Adjacent Bases from  
Average as a Function of Number of Peaks Used as a Reference for  
Alignment of Raw Data

**FIG. 3**



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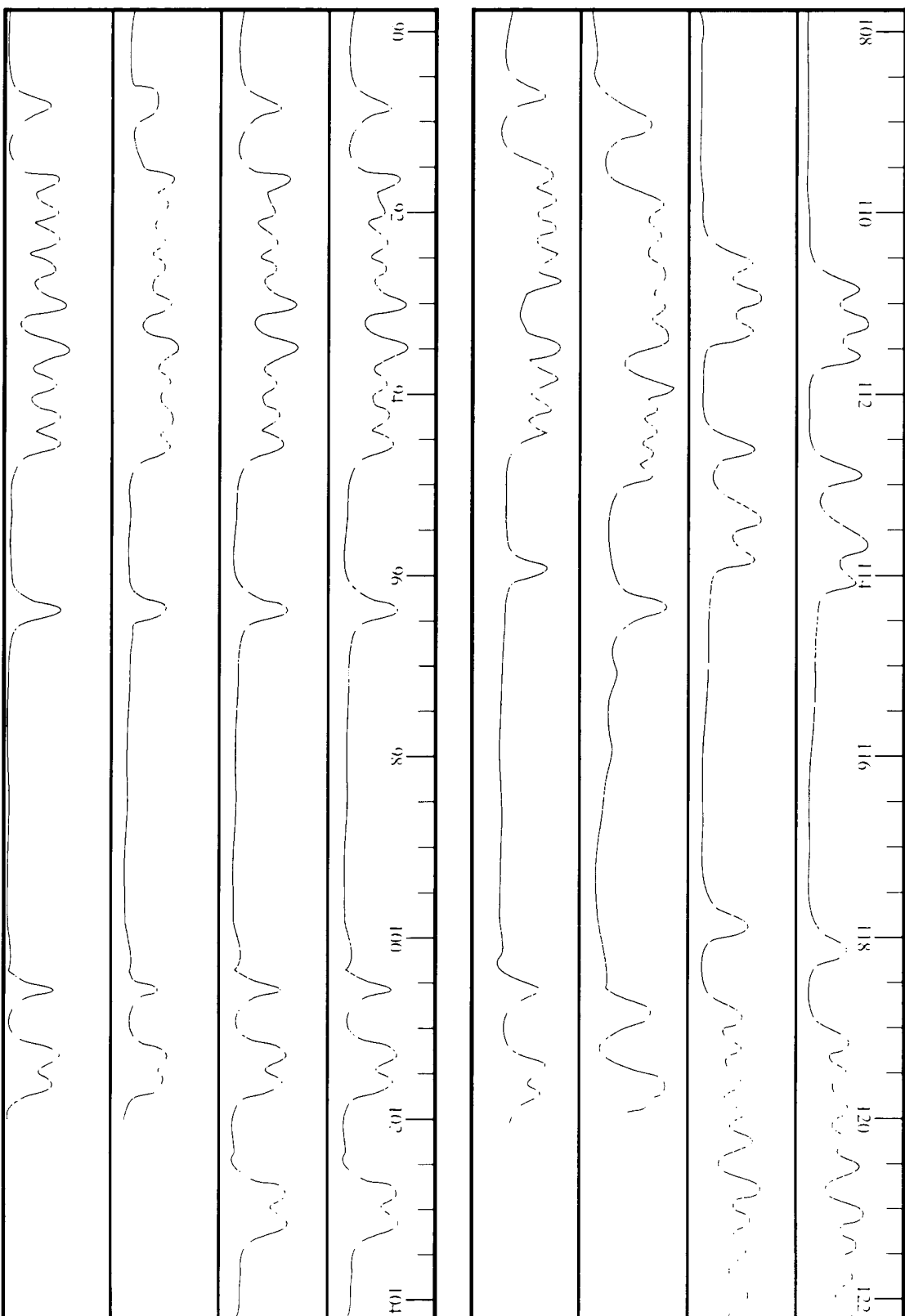
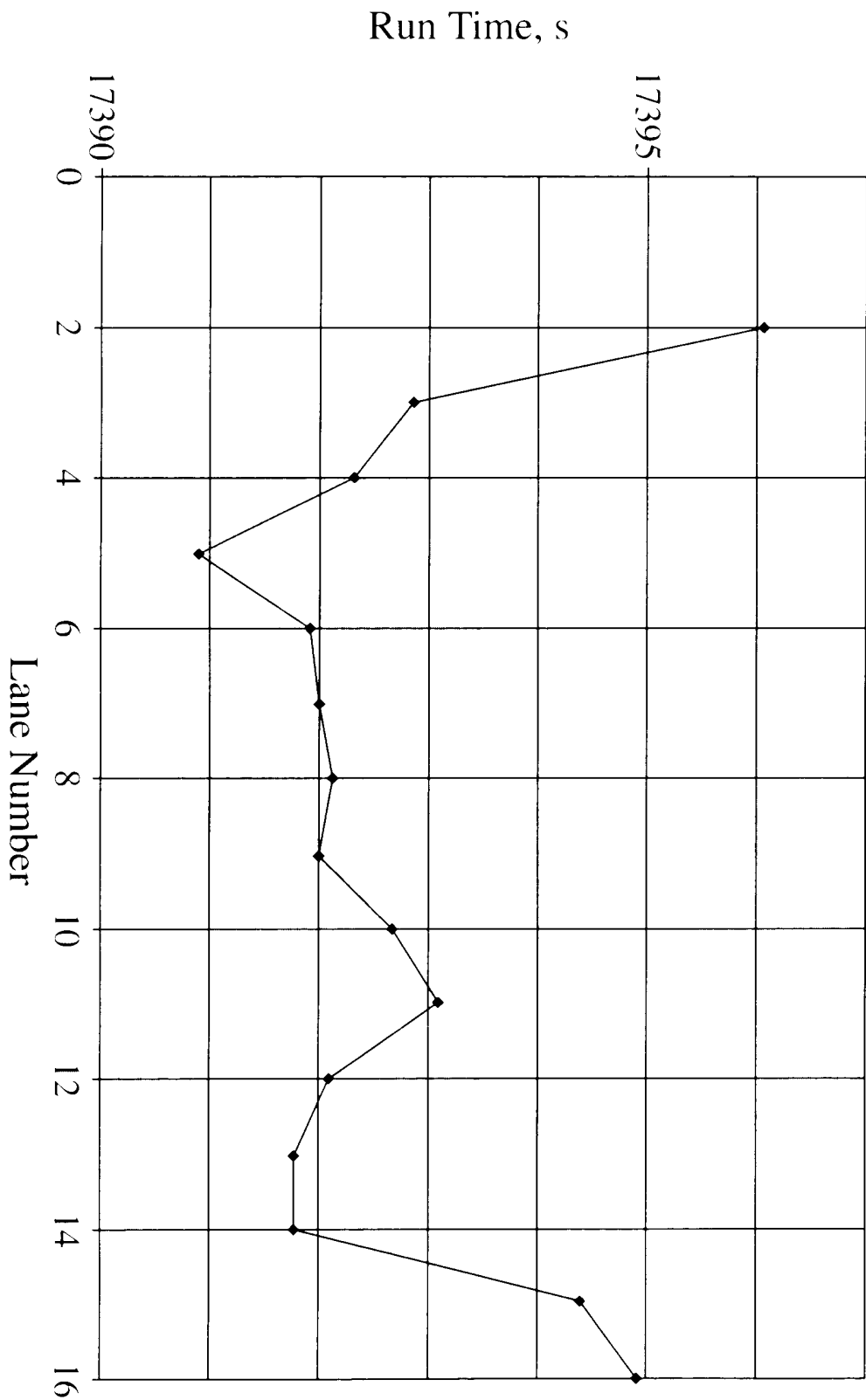


FIG. 4



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**Run Time of the BP#1056 in Different Lanes  
(after alignment based on 10 peaks)**



**FIG. 5**

# HIV-1 TruGene Kit (version 0.80)

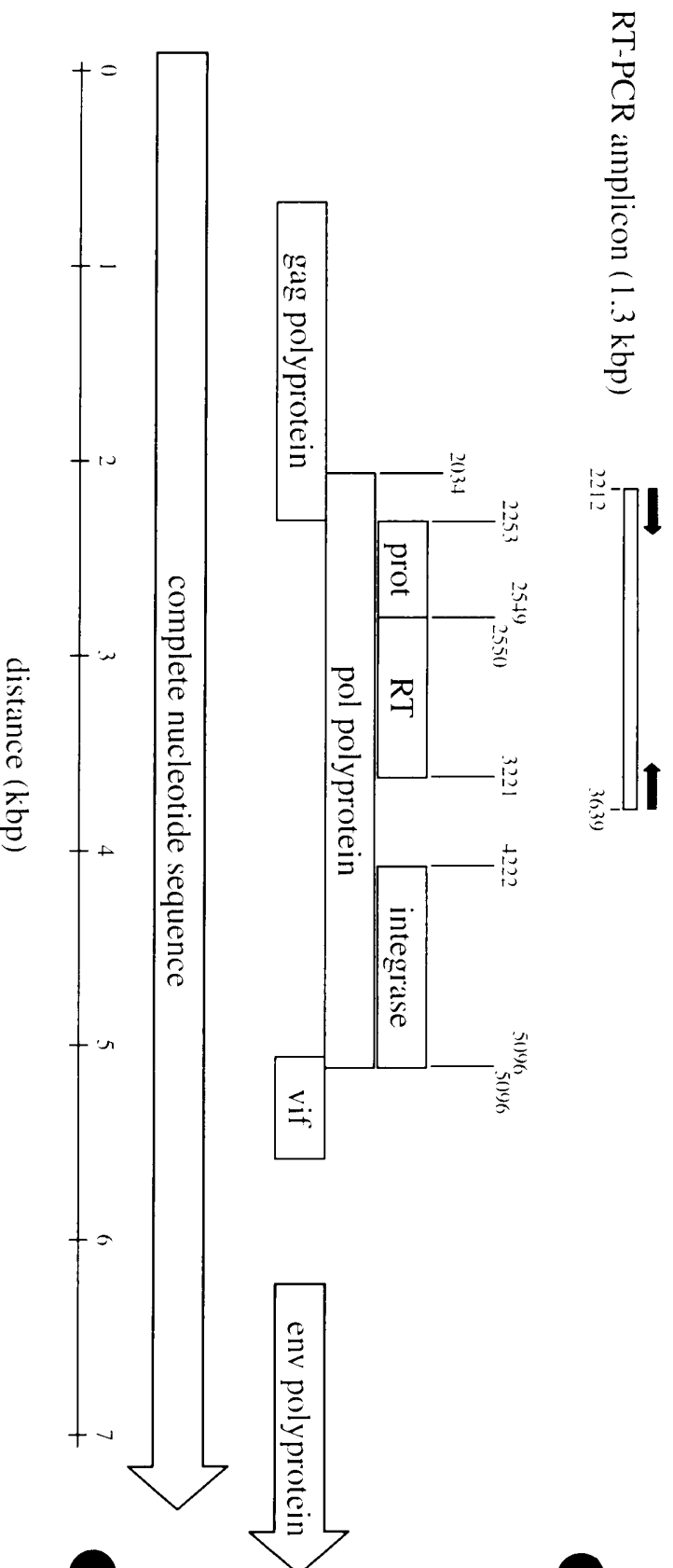


FIG. 6

## Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

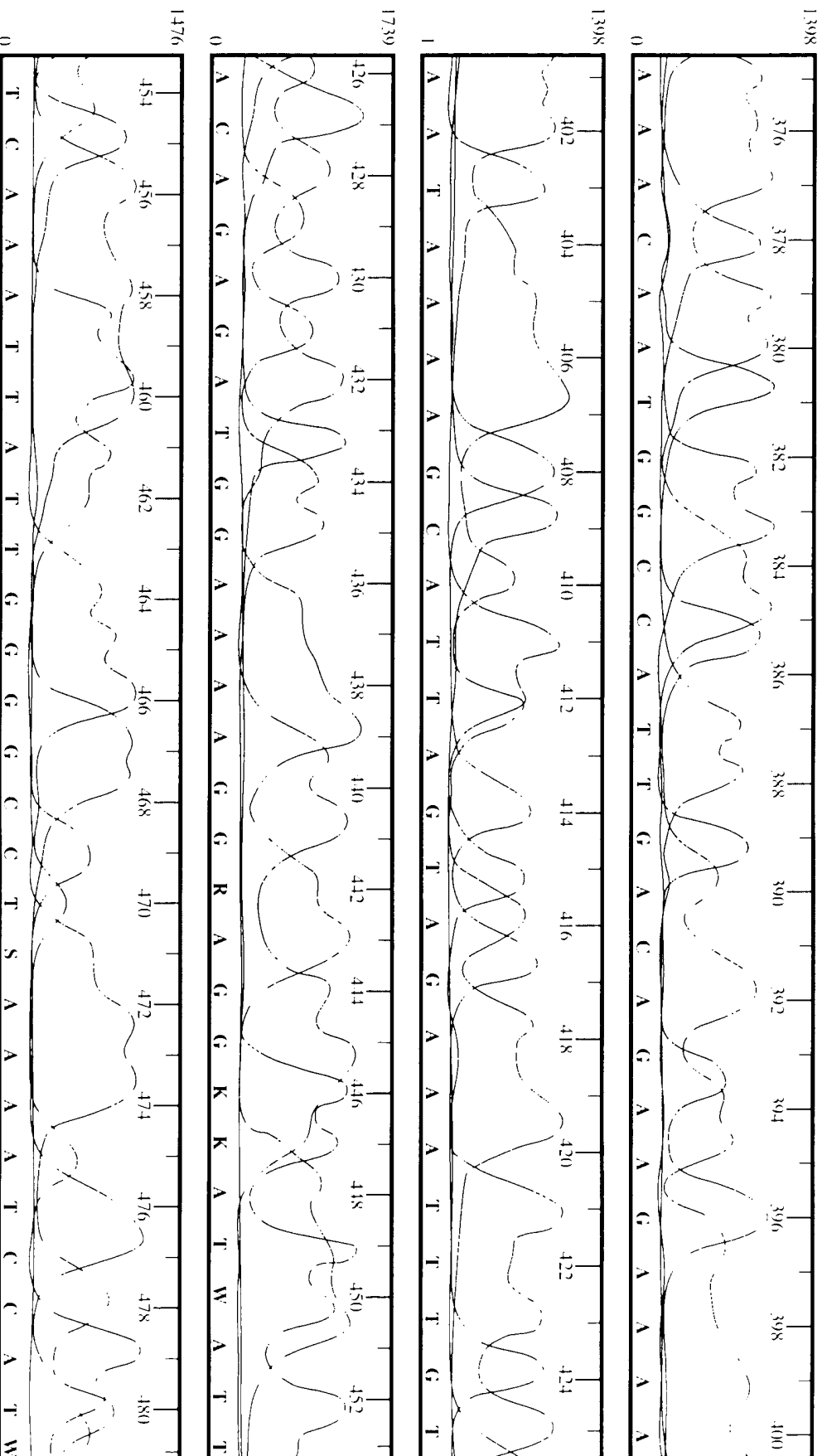
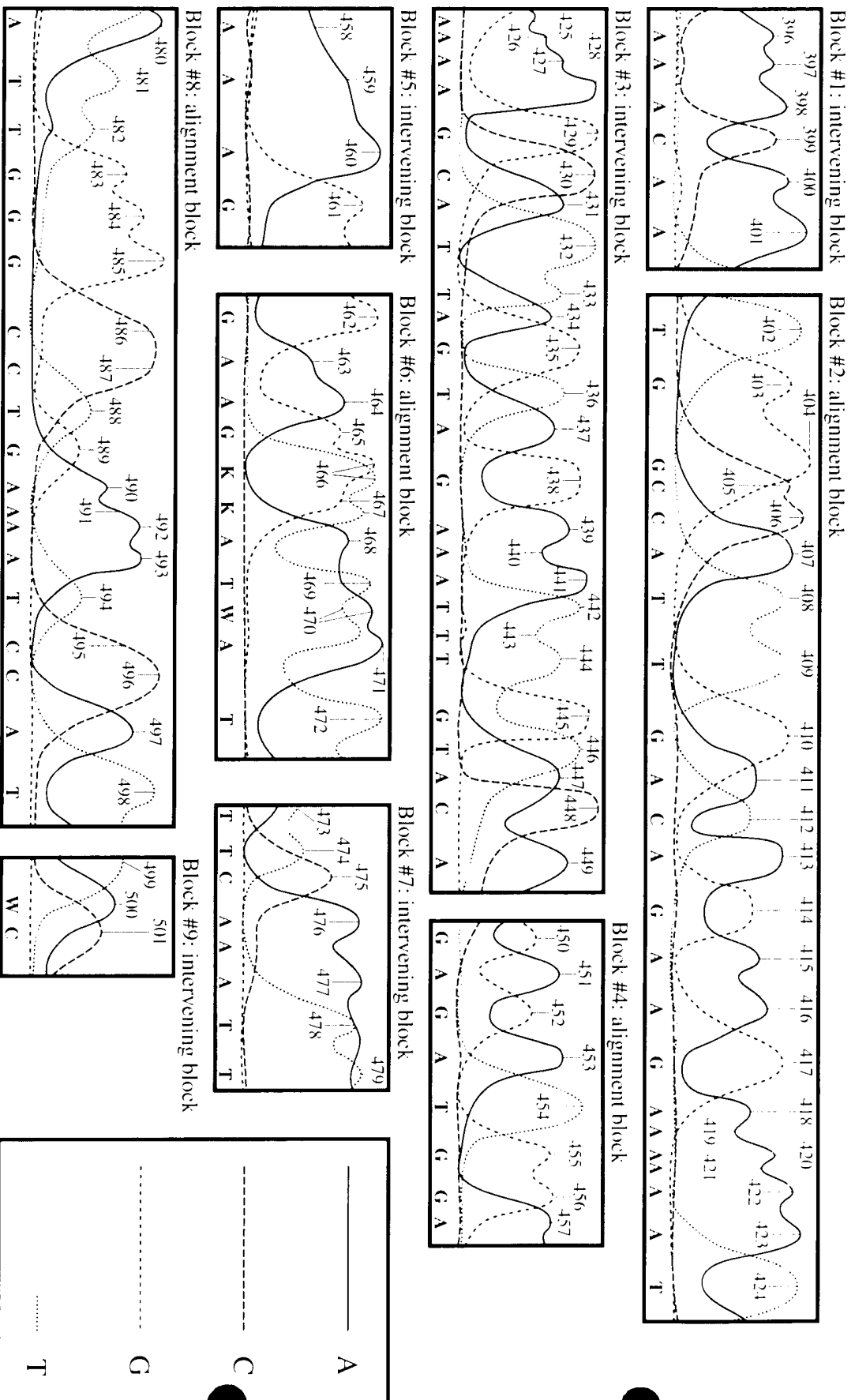


FIG. 7

# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc



**FIG. 8**

# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

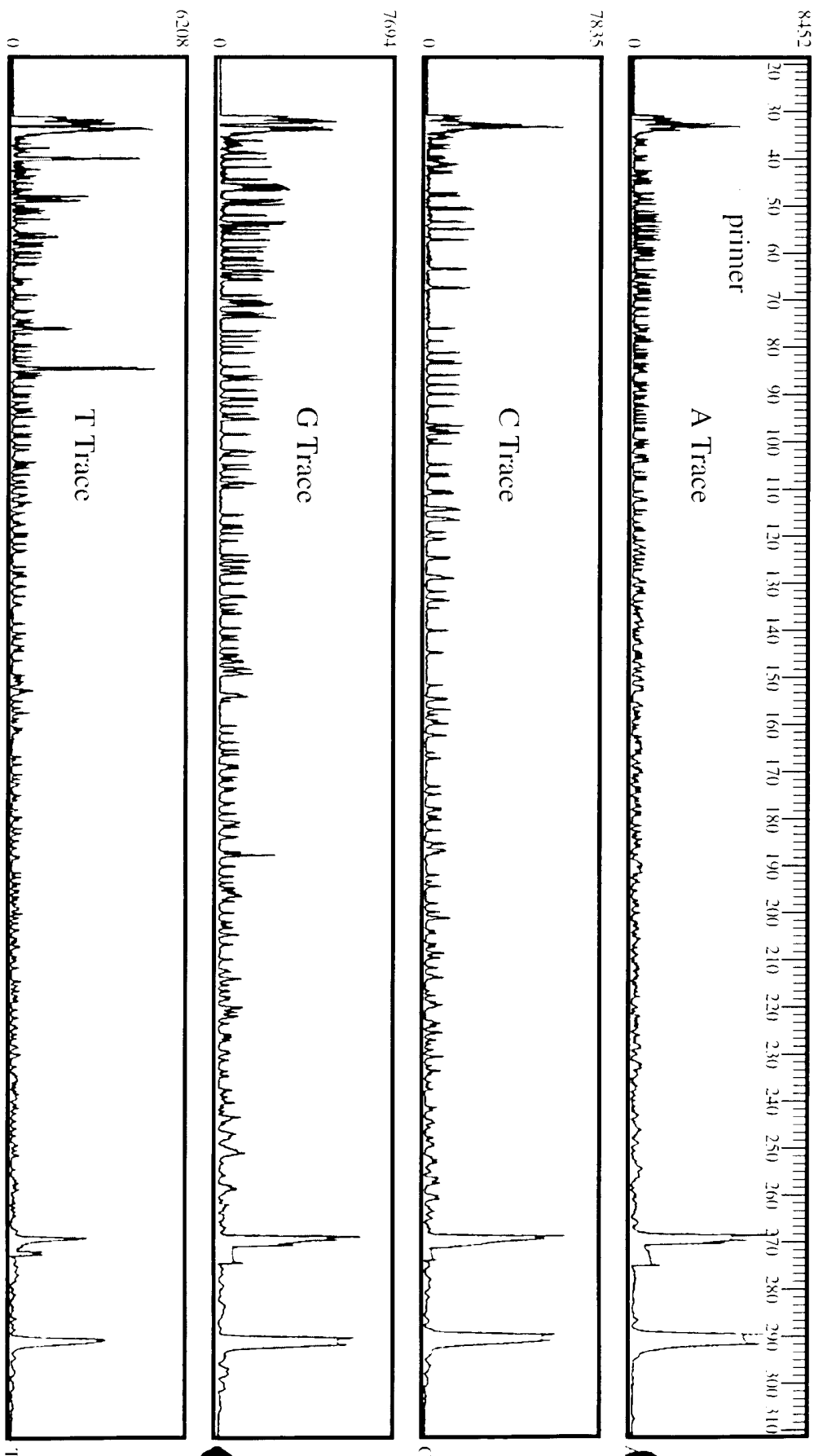


FIG. 9A





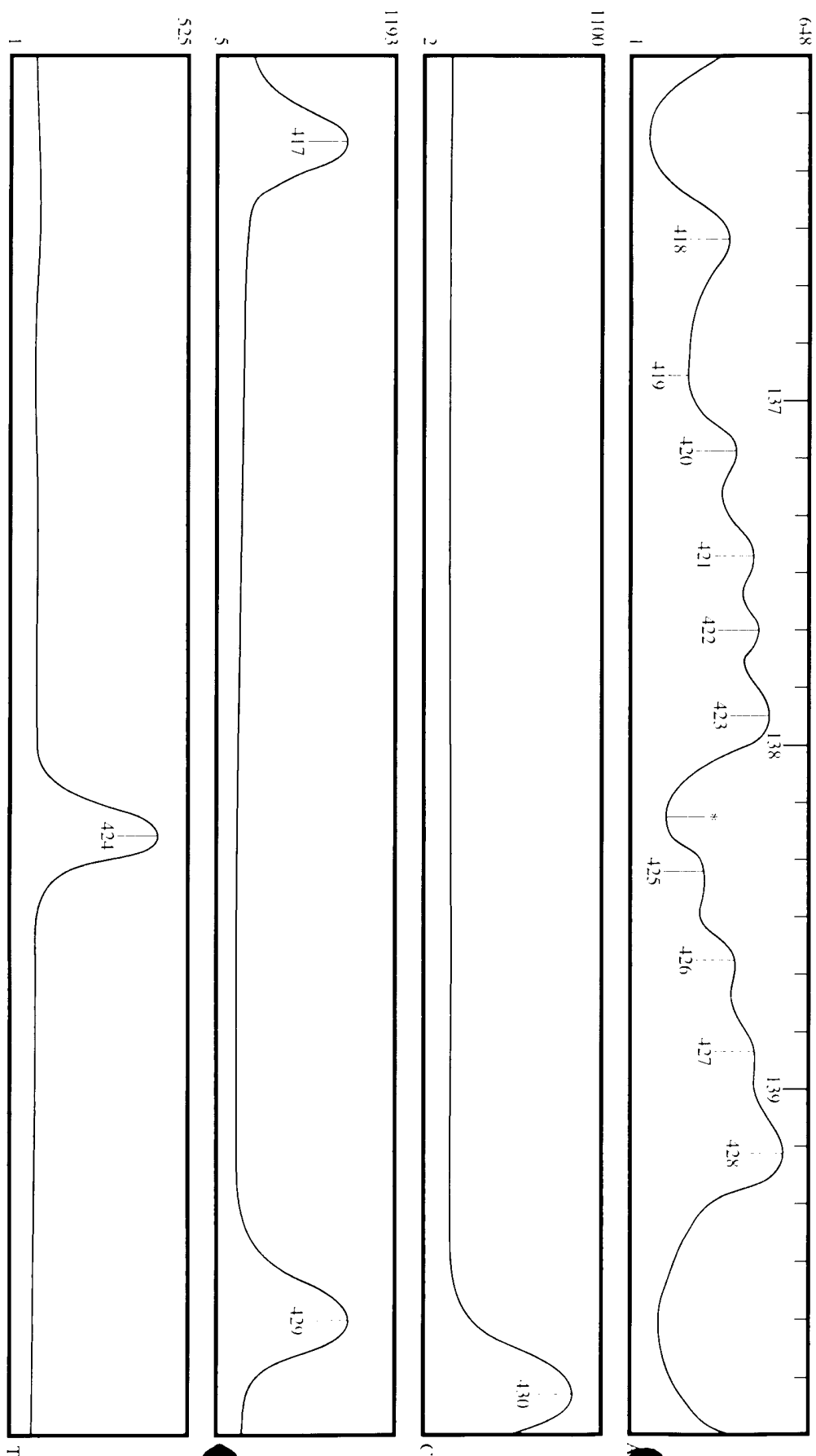


FIG. 9B

## Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

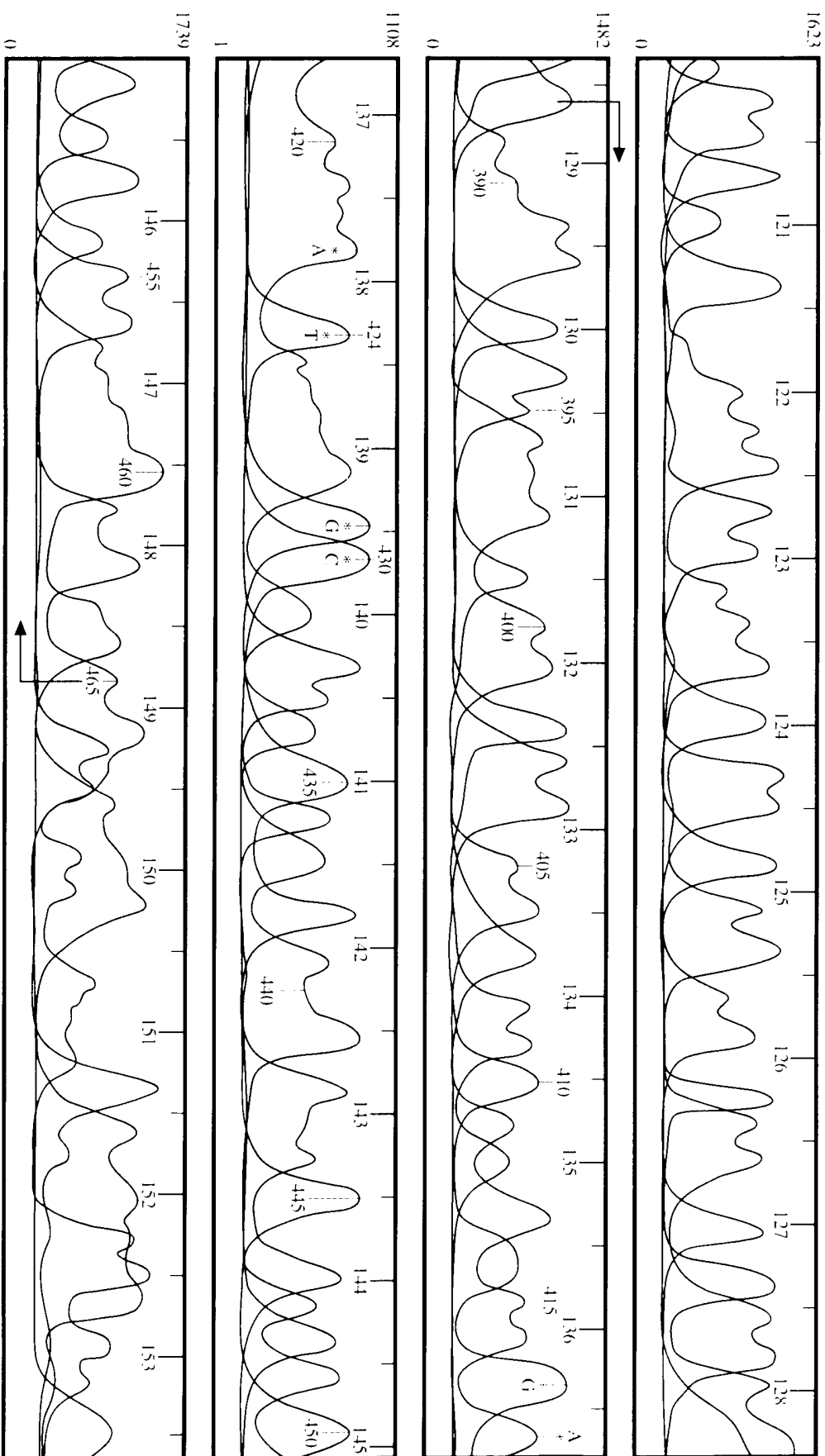


FIG. 9C

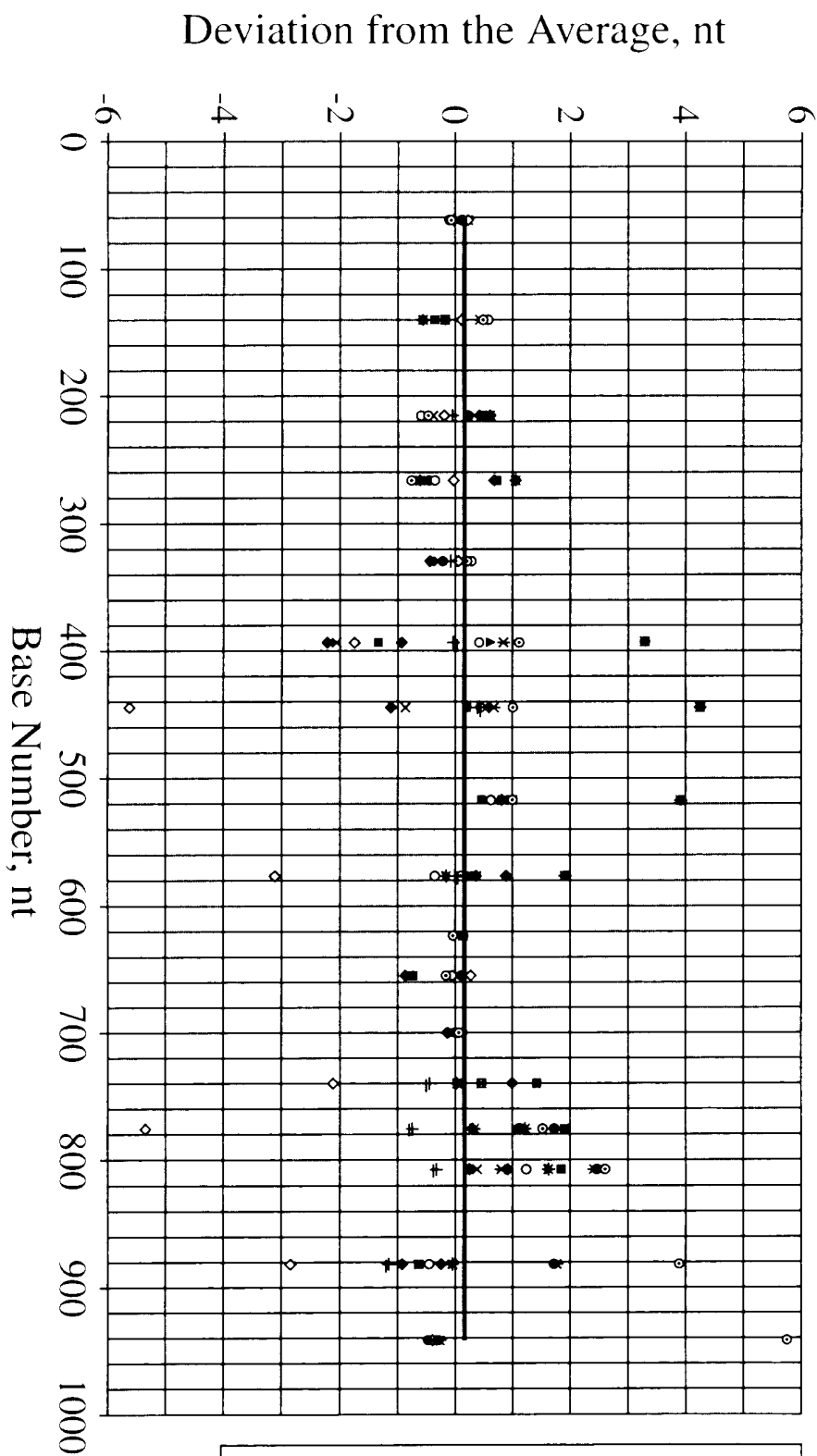
**Deviation of the Peak Position (in Number of Bases) from the Average as a Function of Base Number in Different Traces Before Alignment**

The graph displays the deviation of peak position from the average as a function of base number for 14 different traces. The x-axis represents the Base Number in nucleotides (nt), ranging from 0 to 1000. The y-axis represents the Deviation from the Average in nucleotides (nt), ranging from -200 to 150. A solid black line indicates the average deviation, which remains near zero until approximately base 300, then increases to about 100 nt by base 900. The 14 data series, represented by different markers, show significant scatter, particularly between base 300 and 900, with deviations ranging from approximately -100 nt to +100 nt.

Legend:

- Series1 (filled diamond)
- Series2 (filled square)
- Series3 (filled triangle)
- Series4 (asterisk)
- Series5 (asterisk)
- Series6 (filled circle)
- Series7 (+)
- Series8 (-)
- Series9 (open circle)
- Series10 (open diamond)
- Series11 (open square)
- Series12 (filled diamond)
- Series13 (x)
- Series14 (\*)

**Deviation of the Peak Position from the Average as a Function  
of Base Number in the Traces Aligned with Internal Standards  
(long gel, M13, 6 peaks, 5-th degree polynomial)**



**FIG. 12**